

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 31,796
(C) REFERENCE/DOCKET NUMBER: 22908-0002

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAGCACAGA CTTCAGGTTT CCAAGGAGG ATG GGT GGC TGC AGC ACA AGA GGC
53

Met Gly Gly Cys Ser Thr Arg Gly
1 5

AAG CGG CCG TCA GCC CTC AGT CTG CTG CTG CTG CTG CTC TCG GGG
101

Lys Arg Pro Ser Ala Leu Ser Leu Leu Leu Leu Leu Ser Gly
10 15 20

ATC GCA GCC TCT GCC CTC CCC CTG GAG AGC GGT CCC ACC GGC CAG GAC
149

Ile Ala Ala Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp
25 30 35 40

AGT GTG CAG GAT GCC ACA GGC GGG AGG AGG ACC GGC CTT CTG ACT TTC
197

Ser Val Gln Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe
45 50 55

CTT GCC TGG TGG CAT GAG TGG GCT TCC CAA GAC AGC TCC AGC ACC GCT
245

Leu Ala Trp Trp His Glu Trp Ala Ser Gln Asp Ser Ser Thr Ala
60 65 70

TTC GAA GGG GGT ACC CCG GAG CTG TCT AAG CGG CAG GAA AGA CCA CCC
293

Phe Glu Gly Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro
75 80 85

CTC CAG CAG CCC CCA CAC CGG GAT AAA AAG CCC TGC AAG AAC TTC TTC
341

Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe
90 95 100

TGG AAA ACC TTC TCC TCG AAG TAGCCCGAGC CTGACCGGAG CCTGACCGGC
395

Trp Lys Thr Phe Ser Ser Cys Lys
105 110

CACCCTGTGA ATGCAGCCGT GGCCTGAATA AAGAGTGTCA AGT
438

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Gly Cys Ser Thr Arg Gly Lys Arg Pro Ser Ala Leu Ser Leu
1 5 10 15

Leu Leu Leu Leu Leu Ser Gly Ile Ala Ala Ser Ala Leu Pro Leu
20 25 30

Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln Asp Ala Thr Gly Gly
35 40 45

Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala
50 55 60

Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly Gly Thr Pro Glu Leu
65 70 75 80

Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
85 90 95

Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Cys Ala Leu Ala Ala Leu Cys Ile Val Leu Ala Leu Gly Gly Val
1 5 10 15

Thr Gly Ala Pro Ser Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser
 20 25 30

Leu Ala Ala Ala Thr Gly Lys Gln Glu Leu Ala Lys Tyr Phe Leu Ala
 35 40 45

Glu Leu Leu Ser Glu Pro Asn Gln Thr Glu Asn Asp Ala Leu Glu Pro
 50 55 60

Glu Asp Leu Pro Gln Ala Ala Glu Gln Asp Glu Met Arg Leu Glu Leu
 65 70 75 80

Gln Arg Ser Ala Asn Ser Asn Pro Ala Met Ala Pro Arg Glu Arg Lys
 85 90 95

Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 25..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC
 51

Met Met Gly Gly Arg Gly Thr Gly Gly
 1 5

AAG TGG CCC TCA GCC TTC GGG CTG CTG CTG CTC TGG GGG GTC GCA GCC
 99

Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Trp Gly Val Ala Ala
 10 15 20 25

TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG
 147

Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
 30 35 40

GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG
195

Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
45 50 55

CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT
243

His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
60 65 70

ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC
291

Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
75 80 85

CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC
339

Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
90 95 100 105

TCC TCG TGC AAG TAACCCCCACC CTGGGCATAG CACCCCTGGCC ACCCTGTGAG

391

Ser Ser Cys Lys

110

ATGCCAACGA GACCTGAATA AAGACTGTCA ATCAAAC

427

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Met Gly Gly Arg Gly Thr Gly Gly Lys Trp Pro Ser Ala Phe Gly
1 5 10 15

Leu Leu Leu Leu Trp Gly Val Ala Ala Ser Ala Leu Pro Leu Glu Ser
20 25 30

Gly Pro Thr Gly Gln Asp Ser Val Gln Glu Ala Thr Glu Gly Arg Ser
35 40 45

Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala Ser Gln Ala
50 55 60

Ser Ser Ser Thr Pro Val Gly Gly Thr Pro Gly Leu Ser Lys Ser
65 70 75 80

Gln Glu Arg Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro
85 90 95

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
100 105

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
1 5 10 15
Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp
20 25 30

Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly
35 40 45

Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln
50 55 60

Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr
65 70 75 80

Phe Ser Ser Cys Lys
85

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro
1 5 10 15

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
20 25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
1 5 10 15

Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
20 25 30

His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
35 40 45

Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
50 55 60

Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
65 70 75 80

Ser Ser Cys Lys

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro
1 5 10 15

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
20 25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCGAGATCT AAGGAGGATG GGTGGCTGCA G
31

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTGTCTAGA TCATAGGTCT TCTTCTGATA TTAGTTTTG TTCCTTGAC GAGGAGAAGG
60

TTTTCCAG
68

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCGAGATCT GCCCTCCCCC TGGAGA
26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTGAATTCA GGCCACGGCT GCATTCACAG
30

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Lys Arg Pro Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Trp Pro Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Trp His Glu Trp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCAAGCGGC CGTCAGCC

18

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCAAGTGGC CCTCAGCC

18

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCACCTCA TGCCACCA

18

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Cys Lys Asn Phe Phe Tyr Lys Thr Phe Ser Ser Cys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CC AAAACATTGA TTTCAGGGCT GCCAGGAAGG AAGAGCAGCA GCAGGGTGGG
52

AGAGAAGCTC CAGTCAGCCC ACAAGATGCC ATTGTCCCCC GGCCTCCTGC TGCTGCTGCT
112

CTCCGGGGCC ACGGCCACCG CTGCCCTGCC CCTGGAGGGT GGCCCCACCG GCCGAGACAG
172

CGAGCATATG CAGGAAGCGG CAGGAATAAG GAAAAGCAGC CTCCTGACTT TCCTCGCTTG
232

GTGGTTTGAG TGGACCTCCC AGGCCAGTGC CGGGCCCTC ATAGGAGAGG AAGCCCGGGA
292

GGTGGCCAGG CGGCAGGAAG GCGCACCCCC CCAGCAATCC GCGGCCGGG ACAGAATGCC
352

CTGCAGGAAC TTCTTCTGGA AGACCTTCTC CTCCTGAAA TAAAACCTCA CCCATGAATG
412

CTCACGCAAG TGTAATGACA GACCTGAATA AAATGTATTA AGCAGCAGTG ATCTTCCTC
472

TCCTCCTTCC CAAGTCATTG AAAAGTGTAA GTTATTTAAA TTCCAATAAT GCCCAATACT
532

GACGTGTCTT GAGTAATTG GAACCCAAA GTGAAGATCT TTGATAAAGA TTTTTTTGT
592

GGTCGACTG GACTGTGCTG AGTGCAGGCA CTGGGCTTT CTTCTGATGT TCATTATGGT
652

GCTGGGAAGC TCTGTCTTG ATTTAAAATA AAATAGCTAA AGGCTACAC
701

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Pro Leu Ser Pro Gly Leu Leu Leu Leu Leu Ser Gly Ala Thr
1 5 10 15

Ala Thr Ala Ala Leu Pro Leu Glu Gly Gly Pro Thr Gly Arg Asp Ser
20 25 30

Glu His Met Gln Glu Ala Ala Gly Ile Arg Lys Ser Ser Leu Leu Thr
35 40 45

Phe Leu Ala Trp Trp Phe Glu Trp Thr Ser Gln Ala Ser Ala Gly Pro
50 55 60

Leu Ile Gly Glu Glu Ala Arg Glu Val Ala Arg Arg Gln Glu Gly Ala
65 70 75 80

Pro Pro Gln Gln Ser Ala Arg Arg Asp Arg Met Pro Cys Arg Asn Phe
85 90 95

Phe Trp Lys Thr Phe Ser Ser Cys Lys
100 105

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